AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1-15: (canceled).

Claim 16 (currently amended): A method of ~~specifying~~ identifying a single nucleotide polymorphism (SNP) ~~related to~~ that causes disease susceptibility or [[drug]] responsiveness to a drug [[and]] comprising: ~~a first step of~~

obtaining data from a case group and data from a control group;

defining a ~~continuous~~ scanning domain for a gene thought to cause disease susceptibility or responsiveness to a drug or defining a scanning domain in a genomic region or in one or more chromosomes thought to cause disease susceptibility or responsiveness to a drug;

selecting SNPs to obtain data by SNP haplotyping analysis in the scanning domain;

defining a base sequence domain that contains a specified number of SNPs determined by a range of several SNPs to several [[tens]] hundred SNPs as a window, and shortening the physical distance of the scanning domain by estimating the base sequence domain near a target SNP that causes susceptibility to a disease or responsiveness to a drug by using the data of the selected SNPs; ~~setting a scanning domain beforehand in said window that will be the object of~~

~~SNP analysis~~; ~~a second step of gradually narrowing down said scanning domain to a localized domain that contains a target SNP; and a third step of specifying~~

identifying said target SNP ~~from said narrowed down localized~~ in the shortened scanning domain; and

correlating the target SNP with responsiveness to a drug or with susceptibility to a disease.

Claim 17 (currently amended): The method of ~~specifying SNP of~~ claim 16 wherein said [[second]] step of defining a base sequence domain and shortening the physical distance of the scanning domain comprises defining an SNP near the target SNP with a linkage disequilibrium of the target SNP as a marker SNP, and shortening the physical distance of the scanning domain that contains the marker SNP by calculating differences of a statistical amount data from the case group and data from the control group ~~a step of setting a marker SNP for specifying said target SNP and gradually narrowing down said scanning domain~~.

Claim 18 (currently amended): The method of ~~specifying SNP of~~ claim 17 wherein said [[second]] step of defining a base sequence domain and shortening the physical distance of the scanning domain uses a statistical analysis such as haplotype analysis to [[set]] identify said marker SNP.

Claim 19 (currently amended): The method of ~~specifying SNP of~~ claim 18 wherein said [[first]]

step of defining a base sequence domain and shortening the physical distance of the scanning domain further comprises:

selecting the SNPs to obtain data by SNP typing in the scanning domain, wherein an interval between the selected SNPs is as uniform for the case group and the control group for identifying the target SNP that causes susceptibility to a disease or responsiveness to a drug; ~~a step of setting the scanning domain of said window in a genome domain that is limited to genes whose functions are clearly known or chromosomes whose functions can be predicted; and said second step comprises: a fourth step of selecting a group of SNP to be typed from said scanning domain and performing SNP typing using a wet process; a fifth step of finding~~

calculating the probability of appearance of all combinations of said haplotype analysis in said scanning domain based on typing data of said SNP typing as a statistical amount;

and ~~a sixth step of~~ comparing the ~~found calculated said~~ statistical amount with a preset or estimated reference statistical amount in a position of the window, and when there is a statistically significant ~~deviation~~ value between said statistical amount and said reference statistical amount that exceeds a [[preset]] first threshold value[[,]]; and

determining that said marker SNP is contained in the base sequence domain ~~window corresponding to the deviated position~~ that exceeds said threshold value.

Claim 20 (currently amended): The method of ~~specifying SNP of~~ claim 19 wherein said [[third]] step of identifying said target SNP in the shortened scanning domain further comprises: ~~a seventh step of~~ increasing the ~~specified ratio of the~~ number of selected SNPs having an interval

shorter than a physical distance observed in the linkage disequilibrium when the statistically significant value of the statistical amount is less than a second threshold value of the preset threshold; ~~to be the object of typing in the selection of the SNP group in said fourth step when said significant deviation is less than a first threshold value, and then repeating said fifth step; an eighth step of setting a new scanning domain from said scanning domain that has been decreased by a specified ratio such that it contains the position of the deviated peak when said significant deviation~~

shortening the physical distance of the scanning domain that contains a statistically significant position of the window by a specified ratio when the significant position of a statistically significant value is greater than said [[first]] second threshold value, but less than a ~~second~~ third threshold value[[,]]; and ~~then repeating said fifth step; and a ninth step of~~

determining that said marker SNP is at a position of the window calculated to have the most statistically significant value when the most statistically significant value ~~contained in the domain corresponding to the deviated position that~~ exceeds said second threshold value ~~when said significant deviation exceeds said second threshold value, setting a new scanning domain from said scanning domain that has been decreased by a specified ratio such that it contains the position of the deviated peak, and then repeating said fifth step~~.

Claim 21 (currently amended): The method of ~~specifying SNP of~~ claim 20 wherein said [[ninth]] step of identifying said target SNP in the shortened scanning domain further comprises ~~a step of~~

~~setting~~ identifying SNPs that include the target SNP ~~for which all DNA samples are typed~~ when the number of SNPs in ~~a selected group~~ the selected SNPs is less then a specified number.

Claim 22 (currently amended): The method of ~~specifying SNP of~~ claim 20 wherein said [[seventh]] step of identifying said target SNP in the shortened scanning domain further comprises ~~a step of~~ determining that the target SNP is not contained and stopping the process when the number of times the ~~process of said fifth~~ step of identifying said target SNP in the shortened scanning domain further is performed exceeds a specified number of times.

Claim 23 (canceled).

Claim 24 (currently amended): The method of ~~specifying SNP of~~ claim 16 ~~further defining a continuous domain that contains a specified number of SNPs determined by a range of several to several tens as a window~~, wherein said step of identifying said target SNP in the shortened scanning domain further comprises: finding statistically [[finds]] the probability of appearance of each combination of haplotypes ~~from SNP typing data (all samples)~~ in said window.

Claim 25 (currently amended): The method of ~~specifying SNP of~~ claim 16 wherein the specified number of said SNPs in the window is ten.

Claim 26 (currently amended): The method of ~~specifying SNP of~~ claim 16 wherein the specified

number of said SNPs in the window is three to five.

Claim 27 (currently amended): The method of ~~specifying SNP of~~ claim 16 further comprising moving said window from the start ~~to the end~~ of the [[`]]scanning domain[[`]] to the end of the scanning domain during the processing cycle, and ~~analyzes~~ comparing the statistical amounts between the case group and the control group in the SNP data contained in said window.

Claim 28 (withdrawn): A computer program that can be read by a computer that can execute the processing of the method of specifying SNP of claim 16 wherein all of the steps of claim 16 are coded.